## SEQUENCE LISTING

<110>	SmithKline Beecham Corporation Lambert, Millard H Xu, Robert Wisely , Bruce Collins, Jon												
<120>	CAR LIGAND-BINDING DOMAIN POLYPEPTIDE CO-CRYSTALLIZED WITH A LIGAND, AND METHODS OF DESIGNING LIGANDS THAT MODULATE CAR ACTIVITY												
<130>	PR60235												
<150> <151>	60/488,415 2003-07-18												
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<170>	PatentIn version 3.2												
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	gtgac agccacccca acacgtgacg tc atg gcc agt agg gaa gat gag Met Ala Ser Arg Glu Asp Glu 1	293											
ctg a Leu A	gg aac tgt gtg gta tgt ggg gac caa gcc aca ggc tac cac ttt rg Asn Cys Val Val Cys Gly Asp Gln Ala Thr Gly Tyr His Phe 10 15 20	341											
ASN A	icg ctg act tgt gag ggc tgc aag ggt ttc ttc agg aga aca gtc lla Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Val 85 30 35	389											
agc a Ser l 40	aaa agc att ggt ccc acc tgc ccc ttt gct gga agc tgt gaa gtc Lys Ser Ile Gly Pro Thr Cys Pro Phe Ala Gly Ser Cys Glu Val 45 50 55	437											
agc a Ser i	aag act cag agg cgc cac tgc cca gcc tgc agg ttg cag aag tgc Lys Thr Gln Arg Arg His Cys Pro Ala Cys Arg Leu Gln Lys Cys 60 65 70	485											
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			75					80	2				85				
aca	tta	<b>COO</b>	75 cga	nca	aad	cag			caa	caa	oca	caq		aca	C	ct	581
Ālā	Leu	Arg 90	Arg	Ālā	Lys	GIN	A1a 95	ĞÎñ	Ārģ	Ārģ	Älä	G1n 100	GIII	Thr	· P	ro	
gtg Val	caa Gln 105	ctg Leu	agt Ser	aag Lys	gag Glu	caa Gln 110	gaa Glu	gag Glu	ctg Leu	atc Ile	cgg Arg 115	Inr	ctc Leu	cto Lei	g g	99 1y	629
gcc Ala 120	cac His	acc Thr	cgc Arg	cac His	atg Met 125	ggc Gly	acc Thr	atg Met	ttt Phe	gaa Glu 130	GII	ttt Phe	gtg val	Gli	, ,	tt he .35	677
agg Arg	cct Pro	cca Pro	gct Ala	cat His 140	Leu	ttc Phe	atc Ile	cat His	cac His 145	cag Gln	CCC Pro	ttg Lei	cco Pro	ac Th 15	i. r	tg .eu	725
gcc Ala	cct Pro	gtg Val	ctg Leu 155	Pro	ctg Leu	gtc Val	aca Thr	cac His 160	Pne	gca Ala	gad A Asi	ate	aad Ast 16	, ,,,,	t i	ttc Phe	773
atg Met	gta Val	ctg Lei 170	ı Glr	gto val	ato	aag Lys	ttt Phe 175	Thr	aag Lys	gad	cto Le	g ccu u Pro 18	o va	c tt 1 Ph	e i	cgt Arg	821
tcc Ser	cto Lei 18	Pro	ati	t gaa e Gl	a gad u Asp	cag 61n 190	Ile	tcc Ser	ctt Lei	cte	c aa u Ly 19	S G1	a gc y Al	a go a Al	a	gtg Val	869
gaa Glu 200	ıIl	tg e Cy	t ca s Hi	c at	c gta e Va 20	a ctc l Leu 5	aat Asr	aco Thr	act The	t tt r Ph 21	e cy	t ct s Le	c ca u Gl	a ad n Tl	a nr	caa Gln 215	917
aa Asi	tt n Ph	c ct e Le	c tg u Cy	c gg s G1 22	y Pr	t ctt o Lei	cge Are	tao g Ty	c ac r Th 22	L TI	t ga e Gl	a ga u As	it gg sp G1	ум	cc la 30	cgt Arg	965
gt. Va	9 gg	g tt y Ph	c ca e G1 23	n va	a ga 1 G1	g tti u Pho	t tte	g ga u G1 24	u Le	g ct u Le	c ti u Pł	it ca ne H	ו אַ כּו	ic c ne H 45	at is	gga Gly	1013
ac Th	a ct r Le	a cg u Ar 25	'g L)	ia ct /s Le	g ca eu Gl	g ct n Le	c ca u G1 25	n Gi	g cc u Pr	t ga	ag ta lu T	λı. Λ	tg ci al Lo 60	tc t eu L	tg eu	gct Ala	1061
gc Al	a Me	g gg	cc ct	tc ti eu Pl	tc to ne Se	t cc r Pr 27	O AS	c cg p Ar	a co g Pr	t g	ıy y	tt a al T 75	cc c hr G	ag a ln A	iga krg	gat Asp	1109
ga G1 28	ig at iu I 80	tt ga le A	at c	ag c' ln L	tg ca eu G 21	aa ga In G1 35	g ga u Gl	ig at iu Me	g gg	a c la L 2	tg a eu T 90	ct c hr L	tg c eu G	aa a ln s	igc Ser	tac Tyr 295	1157
a <u>t</u>	tc a	ag g ys G	gc c ly G	In G	ag co ln A 00	ga ag rg Ar	g co	cc cg	rg A	at c sp A 05	gg t rg f	tt c he L	tg t .eu T	yı '	gcg Ala 310	aag Lys	1205
t.	tg c eu L	ta g eu G	ily L	tg c eu L	tg g .eu A	ct ga la G	ag c'	eu A	gg a rg S 20	gc a er 1	itt a	at g Asn (	314 7	icc Ala B25	tac Tyr	ggg Gly	1253

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3												
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cag gag atc tgc agc tgaggccatg ctcacttcct tccccagctc acctggaaca Gln Glu Ile Cys Ser 345	1356											
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Phe Ala Gly Ser Cys Glu Val Ser Lys Thr Gln Arg Arg His Cys Pro 50 60												
Ala Cys Arg Leu Gln Lys Cys Leu Asp Ala Gly Met Arg Lys Asp Met 65 70 75 80												
Ile Leu Ser Ala Glu Ala Leu Ala Leu Arg Arg Ala Lys Gln Ala Gln 85 90 95												
Arg Arg Ala Gln Gln Thr Pro Val Gln Leu Ser Lys Glu Gln Glu Glu 100 105 110												
Leu Ile Arg Thr Leu Leu Gly Ala His Thr Arg His Met Gly Thr Met 115 120 125												
Phe Glu Gln Phe Val Gln Phe Arg Pro Pro Ala His Leu Phe Ile His 130 135 140												
His Gln Pro Leu Pro Thr Leu Ala Pro Val Leu Pro Leu Val Thr His 145 150 155 160												
Phe Ala Asp Ile Asn Thr Phe Met Val Leu Gln Val Ile Lys Phe Thr 165 170 175												

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Lys Asp Leu Pro Val Phe Arg Ser Leu Pro Ile Glu Asp Gln Ile Ser 180 185

Leu Leu Lys Gly Ala Ala Val Glu Ile Cys His Ile Val Leu Asn Thr 195 200 205

Thr Phe Cys Leu Gln Thr Gln Asn Phe Leu Cys Gly Pro Leu Arg Tyr 210 220

Thr Ile Glu Asp Gly Ala Arg Val Gly Phe Gln Val Glu Phe Leu Glu 225 230 235

Leu Leu Phe His Phe His Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu 245 250 255

Pro Glu Tyr Val Leu Leu Ala Ala Met Ala Leu Phe Ser Pro Asp Arg 260 265 270

Pro Gly Val Thr Gln Arg Asp Glu Ile Asp Gln Leu Gln Glu Glu Met 275 280

Ala Leu Thr Leu Gln Ser Tyr Ile Lys Gly Gln Gln Arg Arg Pro Arg 290 295

Asp Arg Phe Leu Tyr Ala Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg 305 310

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DNA

Homo sapiens

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ggg gcc cac acc cgc cac atg ggc acc atg ttt gaa cag ttt gtg cag

48

96

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Gly .	Ala	His	Thr 20	Arg	His	Met	Gly	Thr 25	5 Met	Phe	Glu	Gln	Phe 30	۷a۱	Gln	
ttt Phe	agg Arg	cct Pro 35	cca Pro	gct Ala	cat His	Leŭ	ttc Phe 40	atc Ile	cat His	cac His	cag Gln	CCC Pro 45	ttg Leu	CCC Pro	acc Thr	144
Ctg Leu	gcc Ala 50	cct Pro	gtg Val	ctg Leu	cct Pro	ctg Leu 55	gtc val	aca Thr	cac His	ttc Phe	gca Ala 60	gac Asp	atc Ile	aac Asn	act Thr	192
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cgt Arg	tcc Ser	ctg Leu	ccc Pro	att Ile 85	gaa Glu	gac Asp	cag Gln	atc Ile	tcc ser 90	ctt Leu	ctc Leu	aag Lys	gga Gly	gca Ala 95	gct Ala	288
gtg Val	gaa Glu	atc Ile	tgt Cys 100	cac His	atc Ile	gta Val	ctc Leu	aat Asn 105	acc Thr	act Thr	ttc Phe	tgt Cys	ctc Leu 110	caa Gln	aca Thr	336
caa Gln	aac Asn	ttc Phe 115	ctc Leu	tgc Cys	ggg Gly	cct Pro	ctt Leu 120	cgc Arg	tac Tyr	aca Thr	att Ile	gaa Glu 125	gat Asp	gga Gly	gcc Ala	384
cgt Arg	gtg Val 130	Gly	ttc Phe	cag	gta Val	gag Glu 135	ttt Phe	ttg Leu	gag Glu	ttg Leu	ctc Leu 140	Pne	cac His	ttc Phe	cat His	432
gga Gly 145	Thr	cta Leu	cga Arg	aaa J Lys	ctg Leu 150	Gln	ctc Leu	caa Gln	gag Glu	cct Pro 155	GIU	tat Tyr	gtg Val	Ct C	ttg Leu 160	480
gct Ala	gco	atg Met	gco Ala	cto Leu 16	Phe ي	tct Ser	cct Pro	gac Asp	cga Arg 170	Pro	gga Gly	a gtt ⁄ val	acc Thr	ca Gli 17:	g aga n Arg	528
gat Asp	gag Gli	ati i Ile	ga1 2 Asi 180	o Gli	g ctg n Lei	caa Gln	gag Gli	gag Gli 189	ı met	gca Ala	a ctg a Lei	g act u Thr	cto Lei 190	i GII	a agc n Ser	576
tac Tyr	ato	aaq 2 Ly: 19:	s Gly	c cag	g cag n Glr	g cga n Arg	agg Arg 200	) Pro	cgg Arg	gat g Asp	t cg	g ttt g Phe 209	Lei	ta Ty	t gcg r Ala	624
aag Lys	tte Lei 21	u Lei	a gg u Gl	c ct y Le	g cto u Leo	g gct u Ala 21:	GI	g cto	c cgg u Arg	g age	c at r Il 22	e Asr	gaq 1 Gli	g gc	c tac a Tyr	672
gg G1 22	/ Ty	c ca r Gl	a at n Il	c ca e Gl	g ca n Hi: 23	ș Ile	c ca e Gl	9 99 n G1	c cte	g tc u se 23	r al	c ate	g ate	g t		714
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